FIG 1

ADAMTS-E nucleotide sequence [SEQ ID NO: 1]

CACGCGTCCGACGGCGCGGAGGCCCCGGGCGCGGCGCAGGAGCCCGGTGAT
GCTGCGAAGGCTGTGAACAGGGGAGGCGGCACTGTGGGGGCTGCCGGCAGCCGGGG
CTGGGGAGAGACATGTGGACACGTGGCCTCTATGGCTCCCGCCTGCCAGATCCTCCGC
TGGGCCCTCGCCCTGGGGCTGGGCCTCATGTTCGAGGTCACGCACGCCTTCCGGTCTC
AAGATGAGTTCCTGTCCAGTCTGGAGAGCTATGAGATCGCCTTCCCCACCCGCGTGGAC
CACAACGGGGCACTGCTGGCCTTCTCGCCACCTCCTCCCCGGAGGCAGCGCCGCGGC
ACGGGGGCCACAGCCGAGTCCCGCCTCTTCTACAAAGTGGCCTCGCCCAGCACCCACT
TCCTGCTGAACCTGACCCGCAGCTCCCGTCTACTGGCAGGGCACGTCTCCGTGGAGTA
CTGGACACGGGAGGGCCTGGCCTGGCAGAGGGCGGCCCGGCCCCACTGCCTCTACGC
TGGTCACCTGCAGGGCCAGGCCAGCACCTCCCATGTGGCCATCAGCACCTGTGGAGGC
CTGCACGGCCTGATCGTGGCAGACGAGGAAGAGTACCTGATTGAGCCCCTGCACGGTG
GGCCCAAGGGTTCTCGGAGCCCGGAGGAAAGTGGACCACATGTGGTGTACAAGCGTTC
CTCTCTGCGTCACCCCCACCTGGACACAGCCTGTGGAGTGAGAGATGAGAAACCGTGG
AAAGGGCGGCCATGGTGGCTGCGGACCTTGAAGCCACCGCCTGCCAGGCCCCTGGGG
AATGAAACAGAGCGTGGCCAGCCAGGCCTGAAGCGATCGGTCAGCCGAGAGCGCTACG
TGGAGACCCTGGTGGTGGCTGACAAGATGATGGTGGCCTATCACGGGCGCCGGGATGT
GGAGCAGTATGTCCTGGCCATCATGAACATTGTTGCCAAACTTTTCCAGGACTCGAGTCT
GGGAAGCACCGTTAACATCCTCGTAACTCGCCTCATCCTGCTCACGGAGGACCAGCCCA
CTCTGGAGATCACCCACCATGCCGGGAAGTCCCTGGACAGCTTCTGTAAGTGGCAGAAA
TCCATCGTGAACCACAGCGGCCATGGCAATGCCATTCCAGAGAACGGTGTGGCTAACCA
TGACACAGCAGTGCTCATCACACGCTATGACATCTGCATCTACAAGAACAAACCCTGCG
GCACACTAGGCCTGGCCCCGGTGGGCGGAATGTGTGAGCGCGAGAGAAGCTGCAGCG
TCAATGAGGACATTGGCCTGGCCACAGCGTTCACCATTGCCCACGAGATCGGGCACACA
TTCGGCATGAACCATGACGGCGTGGGAAACAGCTGTGGGGCCCGTGGTCAGGACCCAG
CCAAGCTCATGGCTGCCCACATTACCATGAAGACCAACCCATTCGTGTGGTCATCCTGC
AGCCGTGACTACATCACCAGCTTTCTAGACTCGGGCCTGGGGCTCTGCCTGAACAACCG
GCCCCCCAGACAGGACTTTGTGTACCCGACAGTGGCACCGGGCCAAGCCTACGATGCA
GATGAGCAATGCCGCTTTCAGCATGGAGTCAAATCGCGTCAGTGTAAATACGGGGAGGT
CTGCAGCGAGCTGTGGTGTCTGAGCAAGAGCAACCGGTGCATCACCAACAGCATCCCG
GCCGCCGAGGGCACGCTGTGCCAGACGCACACCATCGACAAGGGGTGGTGCTACAAAC
GGGTCTGTGTCCCCTTTGGGTCGCGCCCAGAGGGTGTGGACGGAGCCTGGGGGCCGT
GGACTCCATGGGGCGACTGCAGCCGGACCTGTGGCGGCGGCGTGTCCTCTTCTAGCC

GTGCAGTGTTCTGAATTTGACAGCATCCCTTTCCGTGGGAAATTCTACAAGTGGAAAACG
TACCGGGGAGGGGGCGTGAAGGCCTGCTCGCTCACGTGCCTAGCGGAAGGCTTCAACT
TCTACACGGAGAGGGCGGCAGCCGTGGTGGACGGGACACCCTGCCGTCCAGACACGG
TGGACATTTGCGTCAGTGGCGAATGCAAGCACGTGGGCTGCGACCGAGTCCTGGGCTC
CGACCTGCGGGAGGACAAGTGCCGAGTGTGTGGCGGTGACGGCAGTGCCTGCGAGAC
CATCGAGGGCGTCTTCAGCCCAGCCTCACCTGGGGCCGGGTACGAGGATGTCGTCTGG
ATTCCCAAAGGCTCCGTCCACATCTTCATCCAGGATCTGAACCTCTCTCTCAGTCACTTG
GCCCTGAAGGGAGACCAGGAGTCCCTGCTGCTGGAGGGGCTGCCCGGGACCCCCCAG
CCCCACCGTCTGCCTCTAGCTGGGACCACCTTTCAACTGCGACAGGGGCCAGACCAGG
TCCAGAGCCTCGAAGCCCTGGGACCGATTAATGCATCTCTCATCGTCATGGTGCTGGCC
CGGACCGAGCTGCCTGCCCTCCGCTACCGCTTCAATGCCCCCATCGCCCGTGACTCGC
TGCCCCCCTACTCCTGGCACTATGCGCCCTGGACCAAGTGCTCGGCCCAGTGTGCAGG
CGGTAGCCAGGTGCAGGCGGTGGAGTGCCGCAACCAGCTGGACAGCTCCGCGGTCGC
CCCCCACTACTCCAGTGCCCACAGCAAGCTGCCCAAAAGGCAGCGCGCCTGCAACACG
GAGCCTTGCCCTCCAGACTGGGTTGTAGGGAACTGGTCGCTCTGCAGCCGCAGCTGCG
ATGCAGGCGTGCGCAGCCGCTCGGTCGTGTGCCAGCGCCGCGTCTCTGCCGCGGAGG
AGAAGGCGCTGGACGACAGCGCATGCCCGCAGCCGCGCCCACCTGTACTGGAGGCCT
GCCACGGCCCCACTTGCCCTCCGGAGTGGGCGGCCCTCGACTGGTCTGAGTGCACCC
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GCGCCACGCTGCCCCCGGCGCACTGCTCACCCGCCGCCAAGCCACCGGCCACCATGC
GCTGCAACTTGCGCCGCTGCCCCCCGGCCCGCTGGGTGGCTGGCGAGTGGGGTGAGT
GCTCTGCACAGTGCGGCGTCGGGCAGCGGCAGCGCTCGGTGCGCTGCACCAGCCACA
CGGGCCAGGCGTCGCACGAGTGCACGGAGGCCCTGCGGCCGCCGACTACCACGCAGC
AGTGTGAGGCCAAGTGCGACAGCCCAACCCCCGGGGACGGCCCTGAAGAGTGCAAGG
ATGTGAACAAGGTCGCCTACTGCCCCCTGGTGCTCAAATTTCAGTTCTGCAGCCGAGCC
TACTTCCGCCAGATGTGCTGCAAAACCTGCCAGGGCCACTAGGGGGCGCGCGGCACCC
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GGCCCCGGGGGGGGCGGGAACTGGGAGGGAAGGGTGAGACGGAGCCGGAAGTTATTT
ATTGGGAACCCCTGCAGGGCCCTGGCTGGGAGGATCCACCCCAACCTCTGCCCTGCCC
GCCCCAGGGGCACCCCGACATCCAGGCCACCCCCTCATGGTGCTACAGACCCTGCCCT
GGGGCCCACACACTCCTGCCAGGAAGCCCTACATCAATAAAGTTCTGTCTTGTGTAGAT
TTCTAAAAAAAAAAAAAAA

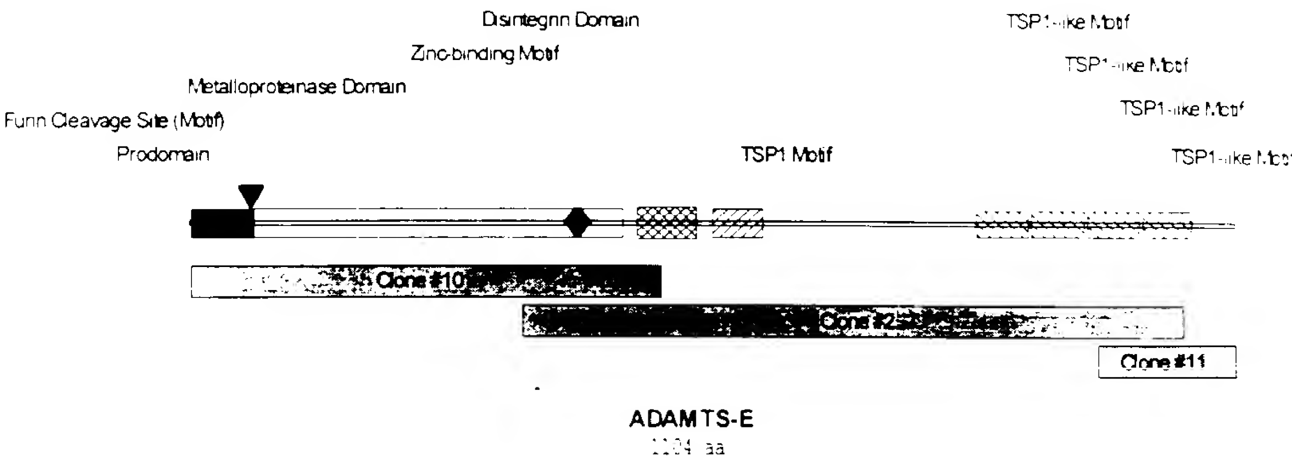
FIG 2

ADAMTS-E amino acid sequence [SEQ ID NO: 2]

MAPACQILRWALALGLGLMFEVTHAFRSQDEFLSSLESYEIAFPTRVDHNGALLAFS
PPPPRRQRRGTGATAESRLFYKVASPSTHFLLNLTRSSRLLAGHVSVEYWTREGLA
WQRAARPHCLYAGHLQGQASTSHVAISTCGGLHGLIVADEEEYLIEPLHGGPKGSR
SPEESGPHVVYKRSSLRHPHLDTACGVRDEKPWKGRPWWLRTLKPPPARPLGNE
TERGQPGLKRSVSRERYVETLVVADKMMVAYHGRRDVEQYVLAIMNIVAKLFQDSS
LGSTVNILVTRLILLTEDQPTLEITHHAGKSLDSFCKWQKSIVNHSGHGNAIPENGVA
NHDTAVLITRYDICIYKNKPCGTLGLAPVGGMCERERSCSVNEDIGLATAFTIAHEIG
HTFGMNHDGVGNSCGARGQDPAKLMAAHITMKTNPFVWSSCSRDYITSFLDSGLG
LCLNNRPPRQDFVYPTVAPGQAYDADEQCRFQHGVKSRQCKYGEVCSELWCLSK
SNRCITNSIPAAEGTLCQTHTIDKGWCYKRVCVPFGSRPEGVDGAWGPWTPWGDC
SRTCGGGVSSSSRHCDSPRPTIGGKYCLGERRRHRSCNTDDCPPGSQDFREVQC
SERDSIPFRCKFYKWKTYRGGGVKACSLTCLAEGFNFYTERAAAVVDGTPCRPDTV
DICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEGVFSPASPGAGYEDV
VWIPKGSVHIFIQDLNLSLSHLALKGDQESLLLEGLPGTPQPHRLPLAGTTFQLRQGP
DQVQSLEALGPINASLIVMVLARTELPALRYRFNAPIARDSLPPYSWHYAPWTKCSA
QCAGGSQVQAVECRNQLDSSAVAPHYCSAHSKLPKRQRACNTEPCPPDWVVGN
WSLCSRSCDAGVRSRSVVCQRRVSAAEEKALDDSACPQPRPPVLEACHGPTCPPE
WAALDWSECTPSCGPGLRHRVVLCKSADHRATLPPAHCSPAAKPPATMRCNLRRC
PPARWVAGEWGECSAQCGVGQRQRSVRCTSHTGQASHECTEALRPPTTTQQCE
AKCDSPTPGDGPEECKDVNKVAYCPLVLKFQFCSRAYFRQMCCKTCQGH

Figure 3. Domain structure of ADAMTS-E and translated nucleic acid sequence. A) Diagram of ADAMTS-E showing the following domains and signature motifs (with amino acid numbers in parentheses): prodomain (1-66), furin cleavage site (63-66), metalloproteinase domain (67-453), zinc-binding motif (392-420), disintegrin domain (469-531), TSP1 motif (548-601), and four TSP1-like motifs (829-884, 888-944, 948-1002, and 1007-1058). Overlapping clones covering the indicated sequence segments are depicted at the bottom of the diagram. **B)** ADAMTS-E nucleotide sequence with translated amino acid sequence above.

A



B

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  1  CACGCGTCCG ACGGCGCGGA GGCCCCGGGC GCGGCGCAGG AGCCCGGTGA TGCTGCGAAG GCTGTGAACA [illegible]
     GTGCGCAGGC TGCCGCGCCT CCGGGGCCCG CGCCGCGTCC TCGGGCCACT ACGACGCTTC CGACACTTGT [illegible]

 +1                                                                     M   A   P   A  [illegible]
                                                                                   Prodomain
                                                                    =====================

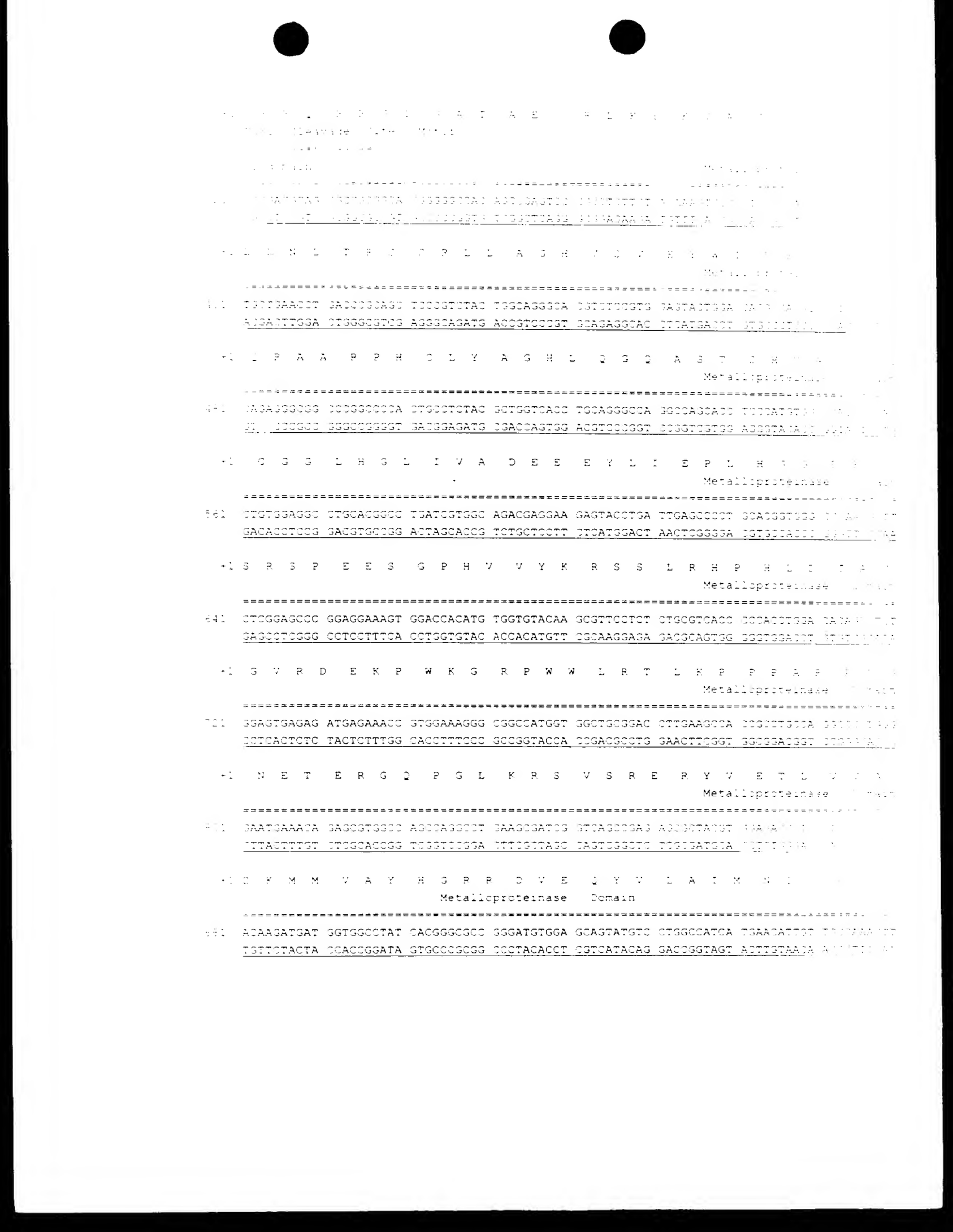
 81  CACTGTGGGG GCTGCCGGCA GCCGGGGCTG GGGAGAGACA TGTGGACACG TGGCCTCTAT GGCTCCCGCC [illegible]
     GTGACACCCC CGACGGCCGT CGGCCCCGAC CCCTCTCTGT ACACCTGTGC ACCGGAGATA CCGAGGGCGG [illegible]

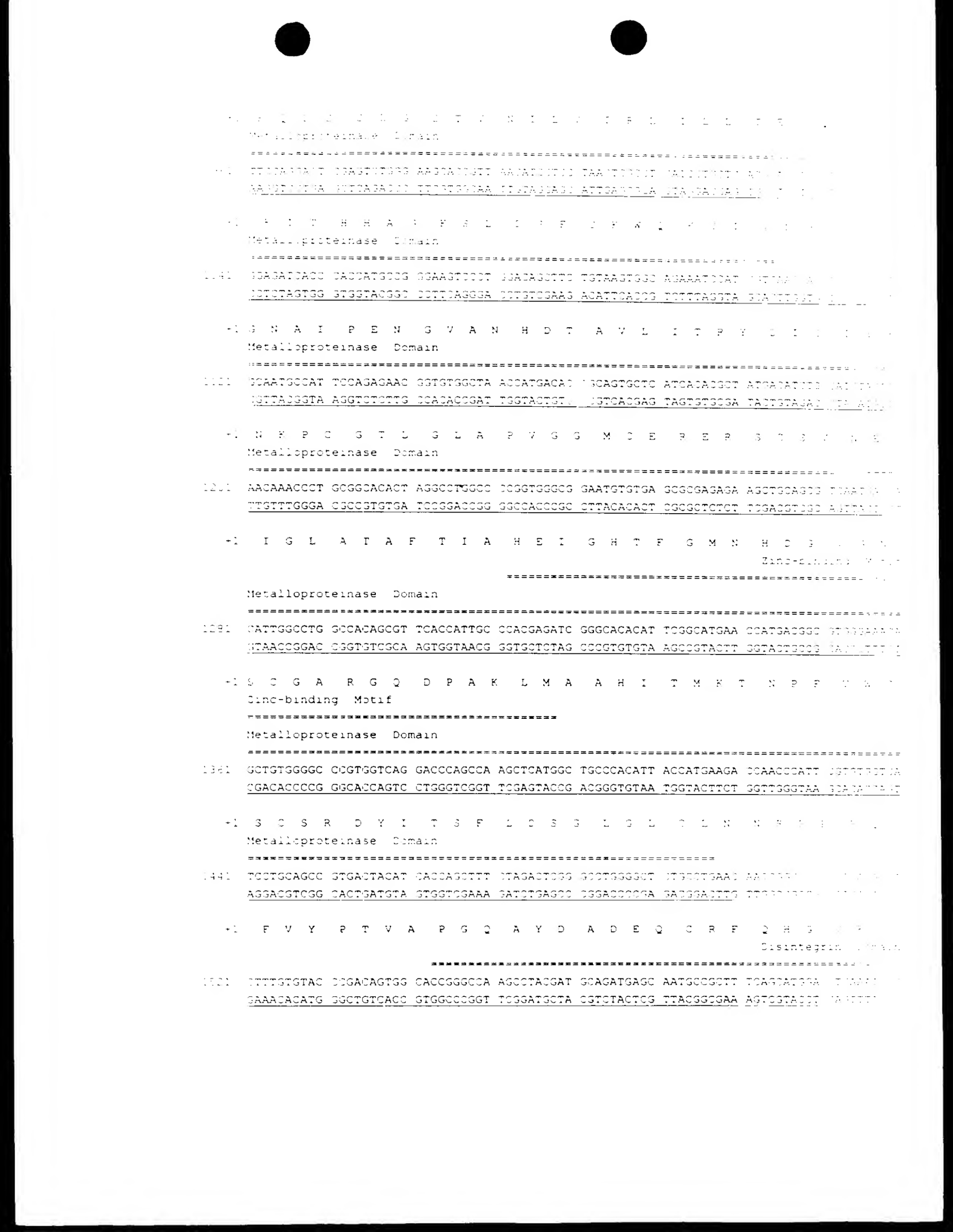
 +1 L   R   W   A   L   A   L   G   L   G   L   M   F   E   V   T   H   A   F   R   S   Q   D   E  [illegible]
                                                                                   Prodomain
    ==========================================================================

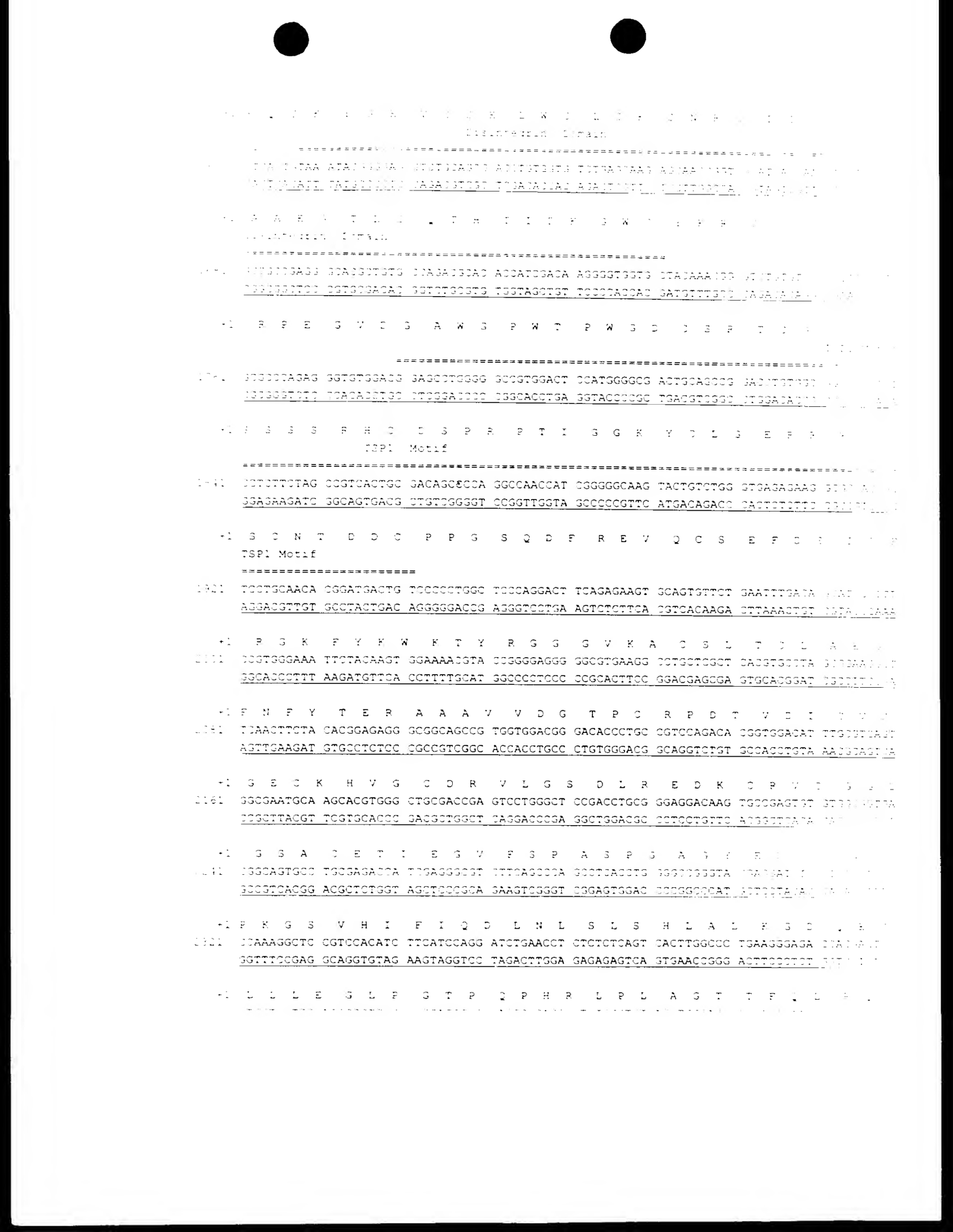
161  TCCGCTGGGC CCTCGCCCTG GGGCTGGGCC TCATGTTCGA GGTCACGCAC GCCTTCCGGT CTCAAGATGA [illegible]
     AGGCGACCCG GGAGCGGGAC CCCGACCCGG AGTACAAGCT CCAGTGCGTG CGGAAGGCCA GAGTTCTACT [illegible]

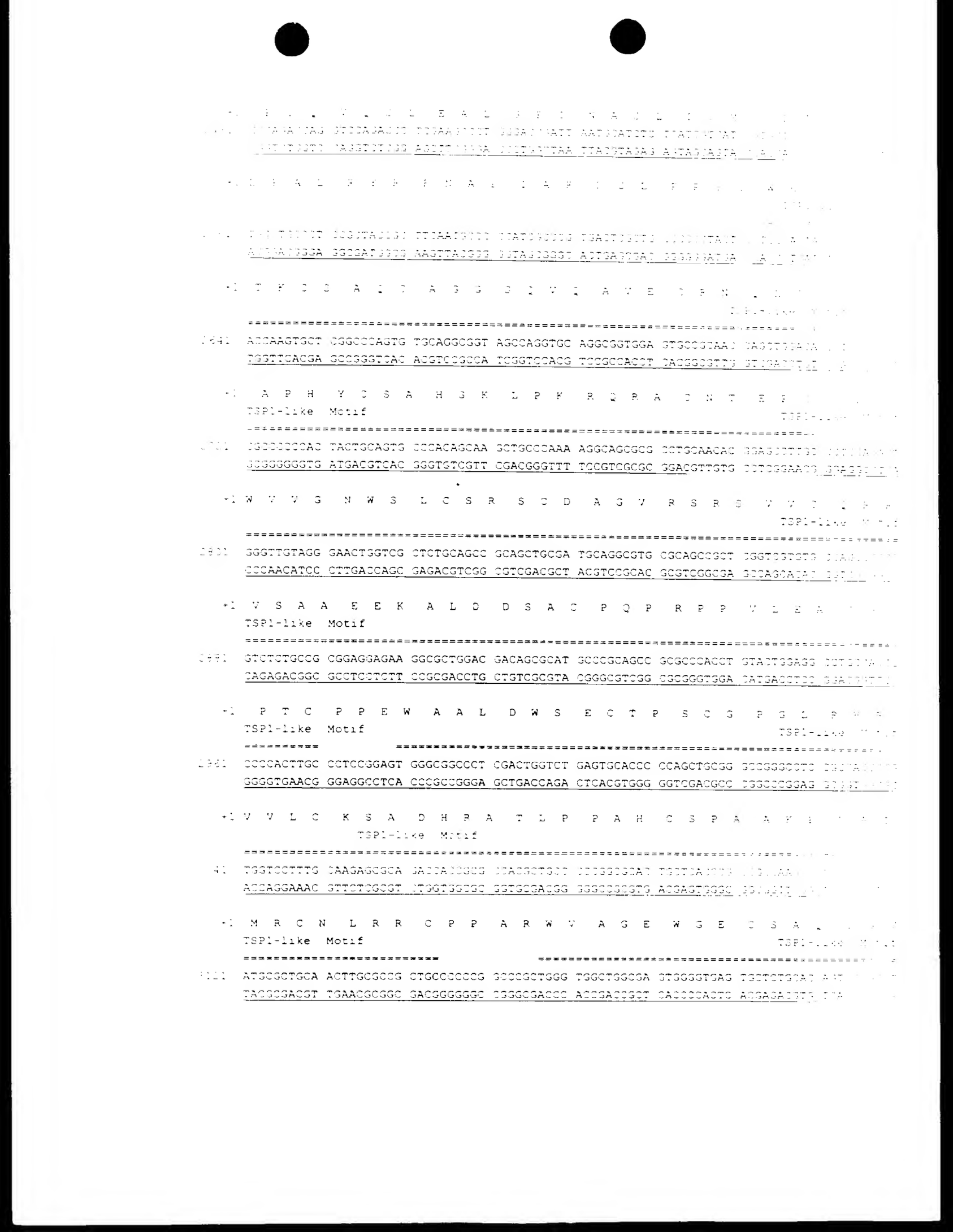
 +1  S   L   E   S   Y   E   I   A   F   P   T   R   V   D   H   N   G   A   L   L   A   F  [illegible]
    Prodomain
    ===================================================================

241  AGTCTGGAGA GCTATGAGAT TGCCTTCCCC ACCCGCGTGG ACCACAACGG GGCACTGCTG [illegible]
     TCAGACCTCT CGATACTCTA GCGGAAGGGG TGGGCGCACC TGGTGTTGCC CCGTGACGAC CGGAAGAGCC [illegible]
```









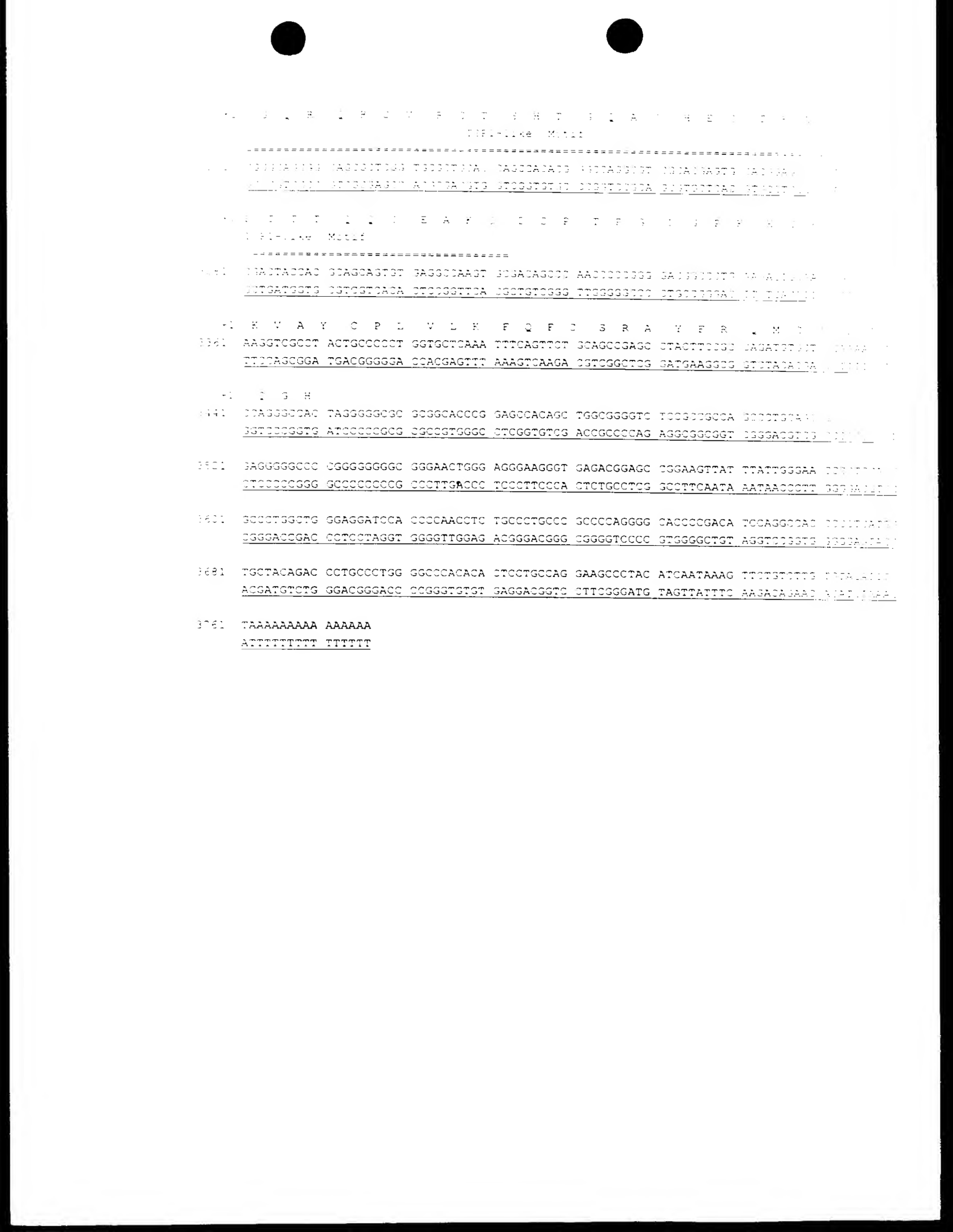
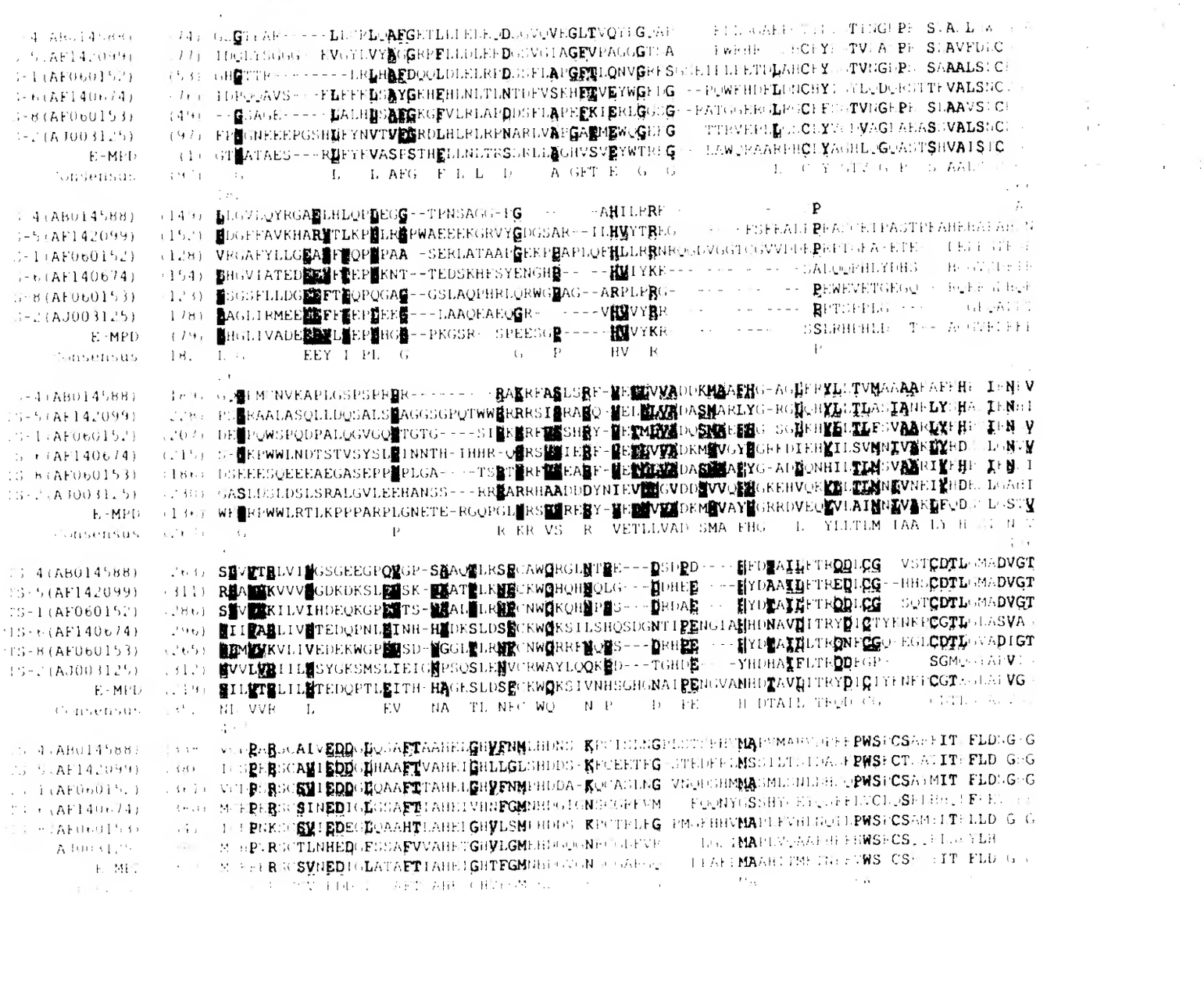


Fig. 4

Metalloproteinase Domain Alignment of ADAMTS-E v. ADAMTS Family



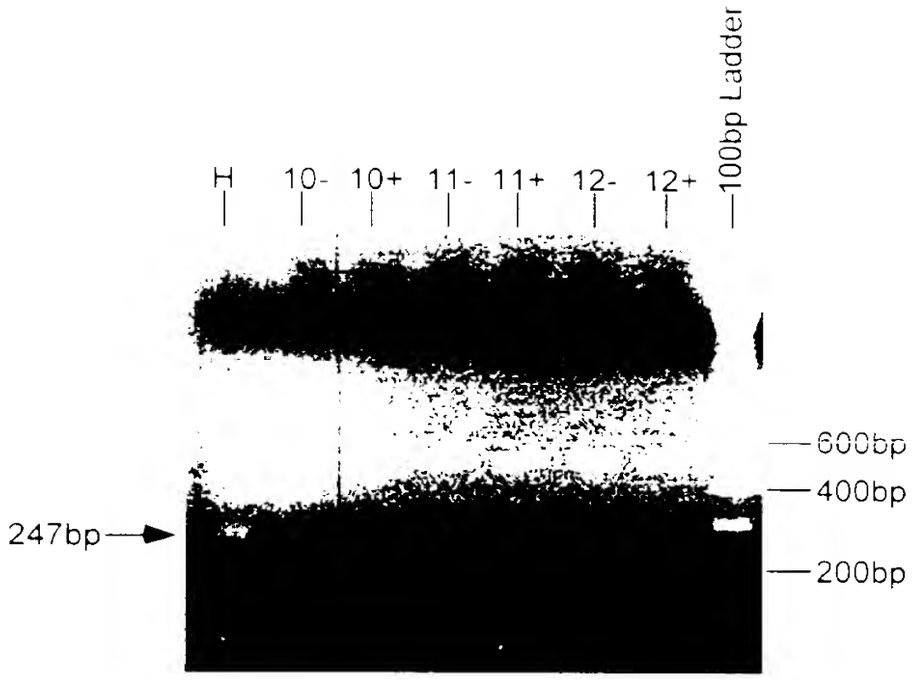


Figure 5. Expression of ADAMTS-E in cDNA from osteoarthritic cartilage.

Figure 6. Amino acid alignment of human ADAMTS-E with a GenScan prediction of ADAMTS-E from mouse genomic sequence.